

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/524,619
Source: PCR
Date Processed by STIC: 3/3/06

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PCT

RAW SEQUENCE LISTING

DATE: 03/03/2006

PATENT APPLICATION: US/10/524,619

TIME: 12:54:53

Input Set : A:\DAVI251.001APC_sequence_listing.TXT

Output Set: N:\CRF4\03032006\J524619.raw

3 <110> APPLICANT: Melbourne Health
 4 Jane, Stephen (US Only)
 5 Wilanowski, Tomasz (US only)
 6 Ting, Stephen (US only)
 8 <120> TITLE OF INVENTION: MAMMALIAN GRAINYHEAD TRANSCRIPTION FACTORS
 10 <130> FILE REFERENCE: DAVI251.001APC
 12 <140> CURRENT APPLICATION NUMBER: US 10/524,619
 13 <141> CURRENT FILING DATE: 2005-02-09
 15 <150> PRIOR APPLICATION NUMBER: PCT/AU03/01006
 16 <151> PRIOR FILING DATE: 2003-08-08
 18 <150> PRIOR APPLICATION NUMBER: US 60/402055
 19 <151> PRIOR FILING DATE: 2002-08-09
 21 <150> PRIOR APPLICATION NUMBER: AU2002951579
 22 <151> PRIOR FILING DATE: 2002-08-22
 24 <160> NUMBER OF SEQ ID NOS: 46
 26 <170> SOFTWARE: PatentIn version 3.1
 28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 1881
 30 <212> TYPE: DNA
 31 <213> ORGANISM: human
 33 <220> FEATURE:
 34 <221> NAME/KEY: CDS
 35 <222> LOCATION: (94)..(1323)
 38 <400> SEQUENCE: 1

39	ataagagagg ccatctgaca gctccagata cgacagtcac tgtctccata gcaacgatgc	60
41	ctacccactc catcaagaca gaaaccacgc cac atg gct tcg ctg tgg gaa tcc	114
42		
43	Met Ala Ser Leu Trp Glu Ser	
45	ccc cag cag tgt atc atc ctg agc cca ctg agc ggg tgg tgg ttt tcg	162
46	Pro Gln Gln Cys Ile Ile Leu Ser Pro Leu Ser Gly Trp Trp Phe Ser	
47	10 15 20	
49	atc gga atc tca ata ctg acc agt tca gct ctg gtg ctc aag ccc caa	210
50	Ile Gly Ile Ser Ile Leu Thr Ser Ser Ala Leu Val Leu Lys Pro Gln	
51	25 30 35	
53	atg ctc aaa ggc gaa ctc cag act cga cct tct cag aga cct tca agg	258
54	Met Leu Lys Gly Glu Leu Gln Thr Arg Pro Ser Gln Arg Pro Ser Arg	
55	40 45 50 55	
57	aag gcg ttc agg agg aac aac ttt gaa tat acc cta gaa gct tca aaa	306
58	Lys Ala Phe Arg Arg Asn Asn Phe Glu Tyr Thr Leu Glu Ala Ser Lys	
59	60 65 70	
61	tca ctt cga cag aag cca gga gac agt acc atg acg tac ctg aac aaa	354
62	Ser Leu Arg Gln Lys Pro Gly Asp Ser Thr Met Thr Tyr Leu Asn Lys	
63	75 80 85	

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65 ggc cag ttc tat ccc atc acc ttg aag gag gtg agc agc agt gaa gga      402
66 Gly Gln Phe Tyr Pro Ile Thr Leu Lys Glu Val Ser Ser Ser Glu Gly
67          90                      95                      100
69 atc cat cat ccc atc agc aaa gtt cga agt gtg atc atg gtg gtt ttt      450
70 Ile His His Pro Ile Ser Lys Val Arg Ser Val Ile Met Val Val Phe
71      105                      110                      115
73 gct gaa gac aaa agc aga gaa gat cag tta agg cat tgg aag tac tgg      498
74 Ala Glu Asp Lys Ser Arg Glu Asp Gln Leu Arg His Trp Lys Tyr Trp
75 120                      125                      130                      135
77 cac tcc cgg cag cac acc gct aaa caa aga tgc att gac ata gct gac      546
78 His Ser Arg Gln His Thr Ala Lys Gln Arg Cys Ile Asp Ile Ala Asp
79          140                      145                      150
81 tat aaa gaa agc ttc aac act atc agt aac atc gag gag att gcg tat      594
82 Tyr Lys Glu Ser Phe Asn Thr Ile Ser Asn Ile Glu Glu Ile Ala Tyr
83          155                      160                      165
85 aac gcc att tcc ttc aca tgg gac atc aac gat gaa gca aag gtt ttc      642
86 Asn Ala Ile Ser Phe Thr Trp Asp Ile Asn Asp Glu Ala Lys Val Phe
87      170                      175                      180
89 atc tct gtc aac tgc tta agc aca gat ttc tct tcc cag aag gga gtg      590
90 Ile Ser Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Val
91      185                      190                      195
93 aag ggg ttg cct ctt aac att caa gtt gat acc tat agt tac aac aac      738
94 Lys Gly Leu Pro Leu Asn Ile Gln Val Asp Thr Tyr Ser Tyr Asn Asn
95 200                      205                      210                      215
97 cgc agc aac aag cct gtg cac cgg gcc tac tgc cag atc aag gtc ttc      786
98 Arg Ser Asn Lys Pro Val His Arg Ala Tyr Cys Gln Ile Lys Val Phe
99          220                      225                      230
101 tgt gac aag gga gct gag cgg aaa atc agg gat gaa gaa cga aag caa      834
102 Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu Glu Arg Lys Gln
103          235                      240                      245
105 agc aaa aga aaa gtt tct gat gtt aaa gtg cca ctg ctt ccc tct cac      882
106 Ser Lys Arg Lys Val Ser Asp Val Lys Val Pro Leu Leu Pro Ser His
107          250                      255                      260
109 aag cga atg gat atc aca gtt ttc aaa ccc ttc att gat ctc gat act      930
110 Lys Arg Met Asp Ile Thr Val Phe Lys Pro Phe Ile Asp Leu Asp Thr
111          265                      270                      275
113 cag cct gtc ctc ttc att cct gac gtg cac ttt gcc aac ttg cag cgg      978
114 Gln Pro Val Leu Phe Ile Pro Asp Val His Phe Ala Asn Leu Gln Arg
115 280                      285                      290                      295
117 ggc act cat gtc ctt ccc att gcc tct gaa gaa ttg gag ggt gaa ggc      1026
118 Gly Thr His Val Leu Pro Ile Ala Ser Glu Glu Leu Glu Gly Glu Gly
119          300                      305                      310
121 tct gtc ttg aaa agg ggg ccg tac ggc aca gaa gat gac ttt gct gtc      1074
122 Ser Val Leu Lys Arg Gly Pro Tyr Gly Thr Glu Asp Asp Phe Ala Val
123          315                      320                      325
125 cct cct tct acc aag ctg gcc cgg ata gaa gaa cca aag aga gtg ctg      1122
126 Pro Pro Ser Thr Lys Leu Ala Arg Ile Glu Glu Pro Lys Arg Val Leu
127          330                      335                      340
129 ctc tac gtt cga aag gag tca gaa gaa gtc ttt gat gcc ctg atg ctc      1170

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130 Leu Tyr Val Arg Lys Glu Ser Glu Glu Val Phe Asp Ala Leu Met Leu
131      345      350      355
133 aaa acc cca tct ttg aag ggc ttg atg gaa gct atc tca gac aaa tac      1218
134 Lys Thr Pro Ser Leu Lys Gly Leu Met Glu Ala Ile Ser Asp Lys Tyr
135 360      365      370      375
137 gat gtt ccc cat gac aag att ggg aaa ata ttc aag aag tgt aaa aag      1266
138 Asp Val Pro His Asp Lys Ile Gly Lys Ile Phe Lys Lys Cys Lys Lys
139      380      385      390
141 ggg atc ctg gtg aac atg gac gac aac att gtg aag cat tac tcc aat      1314
142 Gly Ile Leu Val Asn Met Asp Asp Asn Ile Val Lys His Tyr Ser Asn
143      395      400      405
145 gag gac acc ttccagctgc agattgaaga agccggggggg tcttacaagc      1363
146 Glu Asp Thr
147      410
149 tcaccttgac ggagatctaa aggcctgcgg gccacagctc cccaggagtt cagtgcaggt      1423
151 gtttctagat cttacggttt ggcaactgca ggtaacccca gtcagccatg tcgccagcac      1483
153 aggtctatgt cgagggaatg ggttccttgc aggttgagg cggggctgca tctggcttgg      1543
155 tggtagcatt taatctattg cattggtgtt tttcagatga aagagaaatc catataccat      1603
157 tatgtttgaa tttcctgata tatacaggat ttaagtga aactttattc caagagttaa      1663
159 cagagtctct gggaagcttt aggacatctg ctacgttatt tatcaaaaata ttgggatctc      1723
161 tgccttgatg ctacagtgtc gtgggcctgc tcgctagcag aagtcagaaa aggcgatagg      1783
163 cttggcttta aggatttcgt gcccttgccct gaattcagta caactccact gcctcacggt      1843
165 agcgggagcg cacctgaaga gtacggggggg agccctct      1881
168 <210> SEQ ID NO: 2
169 <211> LENGTH: 410
170 <212> TYPE: PRT
171 <213> ORGANISM: human
173 <400> SEQUENCE: 2
175 Met Ala Ser Leu Trp Glu Ser Pro Gln Gln Cys Ile Ile Leu Ser Pro
176 1      5      10      15
179 Leu Ser Gly Trp Trp Phe Ser Ile Gly Ile Ser Ile Leu Thr Ser Ser
180      20      25      30
183 Ala Leu Val Leu Lys Pro Gln Met Leu Lys Gly Glu Leu Gln Thr Arg
184      35      40      45
187 Pro Ser Gln Arg Pro Ser Arg Lys Ala Phe Arg Arg Asn Asn Phe Glu
188      50      55      60
191 Tyr Thr Leu Glu Ala Ser Lys Ser Leu Arg Gln Lys Pro Gly Asp Ser
192 65      70      75      80
195 Thr Met Thr Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Ile Thr Leu Lys
196      85      90      95
199 Glu Val Ser Ser Ser Glu Gly Ile His His Pro Ile Ser Lys Val Arg
200      100      105      110
203 Ser Val Ile Met Val Val Phe Ala Glu Asp Lys Ser Arg Glu Asp Gln
204      115      120      125
207 Leu Arg His Trp Lys Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln
208      130      135      140
211 Arg Cys Ile Asp Ile Ala Asp Tyr Lys Glu Ser Phe Asn Thr Ile Ser
212 145      150      155      160
215 Asn Ile Glu Glu Ile Ala Tyr Asn Ala Ile Ser Phe Thr Trp Asp Ile

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216          165          170          175
219 Asn Asp Glu Ala Lys Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp
220          180          185          190
223 Phe Ser Ser Gln Lys Gly Val Lys Gly Leu Pro Leu Asn Ile Gln Val
224          195          200          205
227 Asp Thr Tyr Ser Tyr Asn Asn Arg Ser Asn Lys Pro Val His Arg Ala
228          210          215          220
231 Tyr Cys Gln Ile Lys Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile
232 225          230          235          240
235 Arg Asp Glu Glu Arg Lys Gln Ser Lys Arg Lys Val Ser Asp Val Lys
236          245          250          255
239 Val Pro Leu Leu Pro Ser His Lys Arg Met Asp Ile Thr Val Phe Lys
240          260          265          270
243 Pro Phe Ile Asp Leu Asp Thr Gln Pro Val Leu Phe Ile Pro Asp Val
244          275          280          285
247 His Phe Ala Asn Leu Gln Arg Gly Thr His Val Leu Pro Ile Ala Ser
248          290          295          300
251 Glu Glu Leu Glu Gly Glu Gly Ser Val Leu Lys Arg Gly Pro Tyr Gly
252 305          310          315          320
255 Thr Glu Asp Asp Phe Ala Val Pro Pro Ser Thr Lys Leu Ala Arg Ile
256          325          330          335
259 Glu Glu Pro Lys Arg Val Leu Leu Tyr Val Arg Lys Glu Ser Glu Glu
260          340          345          350
263 Val Phe Asp Ala Leu Met Leu Lys Thr Pro Ser Leu Lys Gly Leu Met
264          355          360          365
267 Glu Ala Ile Ser Asp Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys
268          370          375          380
271 Ile Phe Lys Lys Cys Lys Lys Gly Ile Leu Val Asn Met Asp Asp Asn
272 385          390          395          400
275 Ile Val Lys His Tyr Ser Asn Glu Asp Thr
276          405          410
279 <210> SEQ ID NO: 3
280 <211> LENGTH: 2361
281 <212> TYPE: DNA
282 <213> ORGANISM: human
284 <220> FEATURE:
285 <221> NAME/KEY: CDS
286 <222> LOCATION: (7)..(1860)
288 <220> FEATURE:
289 <221> NAME/KEY: VARIANT
290 <222> LOCATION: 342
291 <223> OTHER INFORMATION: Xaa = Lys, Ile
294 <400> SEQUENCE: 3
295 agcgcg atg aca cag gag tac gac aac aaa cgg cca gtg ttg gtt ctt      48
296      Met Thr Gln Glu Tyr Asp Asn Lys Arg Pro Val Leu Val Leu
297      1          5          10
299 cag aat gaa gca ctt tat cca cag cgg cgg tcc tac act agt gag gat      96
300 Gln Asn Glu Ala Leu Tyr Pro Gln Arg Arg Ser Tyr Thr Ser Glu Asp
301 15          20          25          30

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303 gag gcc tgg aaa tcc ttc ctg gaa aac cct ctc act gca gcg acc aaa      144
304 Glu Ala Trp Lys Ser Phe Leu Glu Asn Pro Leu Thr Ala Ala Thr Lys
305          35          40          45
307 gcg atg atg agc atc aat gga gat gaa gac agc gcc gct gcg ctg ggc      192
308 Ala Met Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala Ala Leu Gly
309          50          55          60
311 ctg ctc tat gac tac tac aag gtt cca aga gag aga agg tca tca aca      240
312 Leu Leu Tyr Asp Tyr Tyr Lys Val Pro Arg Glu Arg Arg Ser Ser Thr
313          65          70          75
315 gca aag cca gag gtg gag cac cct gag cca gat cac agc aaa aga aac      288
316 Ala Lys Pro Glu Val Glu His Pro Glu Pro Asp His Ser Lys Arg Asn
317          80          85          90
319 agc ata cca att gtg aca gag cag ccc ctc atc tct gct gga gaa aac      336
320 Ser Ile Pro Ile Val Thr Glu Gln Pro Leu Ile Ser Ala Gly Glu Asn
321 95          100          105          110
323 aga gtg caa gta ctg aaa aat gtg cca ttt aac att gtc ctt ccc cat      384
324 Arg Val Gln Val Leu Lys Asn Val Pro Phe Asn Ile Val Leu Pro His
325          115          120          125
327 ggc aac cag ctg ggc att gat gag aga ggc cat ctg aca gct tca gat      432
328 Gly Asn Gln Leu Gly Ile Asp Lys Arg Gly His Leu Thr Ala Ser Asp
329          130          135          140
331 acg aca gtc act gtc tcc ata gca acg atg cct acc cac tcc atc aag      480
332 Thr Thr Val Thr Val Ser Ile Ala Thr Met Pro Thr His Ser Ile Lys
333          145          150          155
335 aca gaa acc cag cca cat ggc ttc gct gtg gga atc ccc cca gca gtg      528
336 Thr Glu Thr Gln Pro His Gly Phe Ala Val Gly Ile Pro Pro Ala Val
337          160          165          170
339 tat cat cct gag ccc act gag cgg gtg gtg gtt ttc gat cgg aay ctc      576
340 Tyr His Pro Glu Pro Thr Glu Arg Val Val Phe Asp Arg Asn Leu
341 175          180          185          190
343 aat act gac cag ttc agc tct ggt gct caa gcc cca aat gct caa agg      624
344 Asn Thr Asp Gln Phe Ser Ser Gly Ala Gln Ala Pro Asn Ala Gln Arg
345          195          200          205
347 cga act cca gac tcg acc ttc tca gag acc ttc aag gaa ggc gtt cag      672
348 Arg Thr Pro Asp Ser Thr Phe Ser Glu Thr Phe Lys Glu Gly Val Gln
349          210          215          220
351 gag gtt ttc ttc ccc tcg gat ctc agt ctg cgg atg cct ggc atg aat      720
352 Glu Val Phe Phe Pro Ser Asp Leu Ser Leu Arg Met Pro Gly Met Asn
353          225          230          235
355 tca gag gac tat gtt ttt gac agt gtt tct ggg aac aac ttt gaa tat      768
356 Ser Glu Asp Tyr Val Phe Asp Ser Val Ser Gly Asn Asn Phe Glu Tyr
357          240          245          250
359 acc cta gaa gct tca aaa tca ctt cga cag aag cca gga gac agt acc      816
360 Thr Leu Glu Ala Ser Lys Ser Leu Arg Gln Lys Pro Gly Asp Ser Thr
361 255          260          265          270
363 atg acg tac ctg aac aaa ggc cag ttc tat ccc atc acc ttg aag gag      864
364 Met Thr Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Ile Thr Leu Lys Glu
365          275          280          285
367 gtg agc agc agt gaa gga atc cat cat ccc atc agc aaa gtt cga agt      912

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 342
Seq#:4; Xaa Pos. 342
Seq#:7; Xaa Pos. 117,172
Seq#:8; Xaa Pos. 117,172
Seq#:9; N Pos. 2634,2968
Seq#:11; N Pos. 2973,3307
Seq#:15; N Pos. 2806

VERIFICATION SUMMARY

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L:380 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:1056
L:566 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:336
L:1121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:439
L:1133 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:583
L:1290 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:112
L:1302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:160
L:1518 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:2580
L:1530 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:2940
L:1796 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:2940
L:1808 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:3300
L:2427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:2788